

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/762,230

DATE: 06/07/2001

TIME: 11:27:38

Input Set : A:\FUJII Sequence listing.txt

Output Set: C:\CRF3\06072001\I762230.raw

p.s
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C-1>

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3 <110> APPLICANT: FUJII, Tadashi
4     NARITA, Takao
5     NAKATA, Kuniho
6     AGEMATU, Hitosi
7     TSUNEKAWA, Hiroshi
8     ISSHIKI, Kunio
9     YOSHIOKA, Takeo
11 <120> TITLE OF INVENTION: Gene participating in the production of homoglutamic
12     acid and its use
14 <130> FILE REFERENCE: 2001-0116A/LC/00202
16 <140> CURRENT APPLICATION NUMBER: 09/762,230
17 <141> CURRENT FILING DATE: 2001-05-25
19 <150> PRIOR APPLICATION NUMBER: JP10/232382
20 <151> PRIOR FILING DATE: 1998-08-05
22 <150> PRIOR APPLICATION NUMBER: JP11/182362
23 <151> PRIOR FILING DATE: 1999-06-28
25 <160> NUMBER OF SEQ ID NOS: 9
27 <170> SOFTWARE: PatentIn Ver. 2.0
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 2663
31 <212> TYPE: DNA
32 <213> ORGANISM: Flavobacterium lutescens
34 <220> FEATURE:
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36 <222> LOCATION: (801)..(2276)
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43 gtcgccggcag cggcgccctgg gcaatcagtt cgggaggcag gtggtaggca aaatcggact 180
45 tcttcaacgc cggcagctcg atacaacggg ggcgtcagtt tacgccctg taccgcctgt 240
47 gccctcaccg ctcgaaacttg gtgccagga tcaccgccgt ggtggtgcgc tcgaccccat 300
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51 tcgccaccag gtcattgcgc cactgaccg aatgcaggct gcgcaccgca gcaatggcct 420
53 gcagcgcccg caccgaccgc ggcattttct tcggcatcac ggtgatggag atatgcgcgc 480
55 ggacctgctg gcgctccatc gcctggccaa ggcgcacggt gtagccggcg attattccgc 540
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59 ccagcgccgc ggtcgaggcg cgcgcacatc cagcgaacag gtcaagcaac tgtgcatccg 660
61 cctgggaaat ggtaactttg tcgaaaacct ttcgtcaatc cgccgaaacc ggccattgat 720
63 ttgagcagat tcgcactgcc atttgtagtg cgttaacggt tacaactaac actagacaca 780
65 atcagcacgg attcagcatg tcc ctt ctt gcc ccg ctc gcc ccg ctc cgc gcc 833
66                               Ser Leu Leu Ala Pro Leu Ala Pro Leu Arg Ala
67                               1           5           10
69 cat gcc ggc acc cgc ctt acc cag ggc ctg tct gac ccg cag gtc gag 881
70 His Ala Gly Thr Arg Leu Thr Gln Gly Leu Ser Asp Pro Gln Val Glu
71                               15           20           25
73 cag ctg gcc gcc aac cac cct gac ctg cgc gcc gcc atc gac gcc gct 929
74 Gln Leu Ala Ala Asn His Pro Asp Leu Arg Ala Ala Ile Asp Ala Ala

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77 gcc gac gaa tac gcg cgc atc aaa ccg cag gcc gcg gca ttg ctg gac 977
78 Ala Asp Glu Tyr Ala Arg Ile Lys Pro Gln Ala Ala Leu Leu Asp
79          45          50          55
81 ctg gat gaa agc gcg cag atc gcc gcc gtg cag gat ggc ttc gtc aac 1025
82 Leu Asp Glu Ser Ala Gln Ile Ala Ala Val Gln Asp Gly Phe Val Asn
83 60          65          70          75
85 ttc tat gcc gat gat gcg gtg gtg ccc tat atc gcc ctg gcc gcc cgc 1073
86 Phe Tyr Ala Asp Asp Ala Val Val Pro Tyr Ile Ala Leu Ala Ala Arg
87          80          85          90
89 ggg ccg tgg gtg gtc agc ctg aag ggc gcg gtg ctg tat gac gcc ggc 1121
90 Gly Pro Trp Val Val Ser Leu Lys Gly Ala Val Leu Tyr Asp Ala Gly
91          95          100          105
93 ggc tac ggc atg ctc ggc ttc ggc cat acc ccg gcc gat atc ctg gag 1169
94 Gly Tyr Gly Met Leu Gly Phe Gly His Thr Pro Ala Asp Ile Leu Glu
95          110          115          120
97 gcg gtc ggc aag ccg cag gtg atg gcc aac atc atg act ccc tcg ctg 1217
98 Ala Val Gly Lys Pro Gln Val Met Ala Asn Ile Met Thr Pro Ser Leu
99          125          130          135
101 gcc cag ggc cgc ttc att gcc gca atg cgc cgc gaa atc ggc cat acc 1265
102 Ala Gln Gly Arg Phe Ile Ala Ala Met Arg Arg Glu Ile Gly His Thr
103 140          145          150          155
105 cgc ggc ggc tgc ccg ttc tcg cac ttc atg tgc ctg aac tcc ggc tcc 1313
106 Arg Gly Gly Cys Pro Phe Ser His Phe Met Cys Leu Asn Ser Gly Ser
107          160          165          170
109 gaa gcg gtc ggg ctg gcc gcg cgc atc gcc gac atc aac gcc aag ctg 1361
110 Glu Ala Val Gly Leu Ala Ala Arg Ile Ala Asp Ile Asn Ala Lys Leu
111          175          180          185
113 atg acc gac ccg ggc gcc cgg cat gcc ggc gcc acg atc aag cgc gtg 1409
114 Met Thr Asp Pro Gly Ala Arg His Ala Gly Ala Thr Ile Lys Arg Val
115          190          195          200
117 gtg atc aag ggc agt ttc cac ggc cgt acc gac cgt ccg gcg ctg tat 1457
118 Val Ile Lys Gly Ser Phe His Gly Arg Thr Asp Arg Pro Ala Leu Tyr
119          205          210          215
121 tcc gat tcc acc cgc aag gcc tac gat gcg cat ctg gcc agc tac cgc 1505
122 Ser Asp Ser Thr Arg Lys Ala Tyr Asp Ala His Leu Ala Ser Tyr Arg
123 220          225          230          235
125 gac gag cac agc gtc att gcc atc gcc ccg tat gac cag cag gcc ctg 1553
126 Asp Glu His Ser Val Ile Ala Ile Ala Pro Tyr Asp Gln Gln Ala Leu
127          240          245          250
129 cgc cag gtg ttt gcc gat gcc cag gcc aac cac tgg ttc atc gag gcg 1601
130 Arg Gln Val Phe Ala Asp Ala Gln Ala Asn His Trp Phe Ile Glu Ala
131          255          260          265
133 gtg ttc ctg gag ccg gtg atg ggc gaa ggc gac ccg ggc cgt gcg gtg 1649
134 Val Phe Leu Glu Pro Val Met Gly Glu Gly Asp Pro Gly Arg Ala Val
135          270          275          280
137 ccg gtg gac ttc tac cgc ctg gcc cgt gag ctg acc cgc gaa cac ggc 1697
138 Pro Val Asp Phe Tyr Arg Leu Ala Arg Glu Leu Thr Arg Glu His Gly
139          285          290          295

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141 agc ctg ctg ctg atc gat tcg atc cag gcc gcg ctg cgc gtg cac ggc 1745
142 Ser Leu Leu Leu Ile Asp Ser Ile Gln Ala Ala Leu Arg Val His Gly
143 300 305 310 315
145 acc ctg tcc ttc gtc gac tac ccc ggc cac cag gag ctg gag gca ccg 1793
146 Thr Leu Ser Phe Val Asp Tyr Pro Gly His Gln Glu Leu Glu Ala Pro
147 320 325 330
149 gac atg gag acc tac tcc aag gcc ctg aac ggc gcc cag ttc ccg ctg 1841
150 Asp Met Glu Thr Tyr Ser Lys Ala Leu Asn Gly Ala Gln Phe Pro Leu
151 335 340 345
153 tcg gta gtg gcc gtg acc gag cac gcc gcc gcg ctg tac cgc aag ggc 1889
154 Ser Val Val Ala Val Thr Glu His Ala Ala Ala Leu Tyr Arg Lys Gly
155 350 355 360
157 gtg tac ggc aac acc atg acc acc aac ccg cgg gcg ctg gac gtg gcc 1937
158 Val Tyr Gly Asn Thr Met Thr Thr Asn Pro Arg Ala Leu Asp Val Ala
159 365 370 375
161 tgc gcc acc ctg gca cgc ctg gat gag ccg gtc cgc aac aat atc cgc 1985
162 Cys Ala Thr Leu Ala Arg Leu Asp Glu Pro Val Arg Asn Asn Ile Arg
163 380 385 390 395
165 ctg cgt ggc cag cag gcg atg cag aag ctg gaa gca ttg aag gaa ccg 2033
166 Leu Arg Gly Gln Gln Ala Met Gln Lys Leu Glu Ala Leu Lys Glu Arg
167 400 405 410
169 ctg ggg ggc gcg atc acc aag gtg cag ggc acc ggc ctg ctg ttc tcc 2081
170 Leu Gly Gly Ala Ile Thr Lys Val Gln Gly Thr Gly Leu Leu Phe Ser
171 415 420 425
173 tgc gag ctg gcc ccg cag tac aag tgc tac ggg gcc ggc tcc acc gag 2129
174 Cys Glu Leu Ala Pro Gln Tyr Lys Cys Tyr Gly Ala Gly Ser Thr Glu
175 430 435 440
177 gag tgg ctg cgc atg cac ggg gtc aat gtg atc cac ggc ggc gag aat 2177
178 Glu Trp Leu Arg Met His Gly Val Asn Val Ile His Gly Gly Glu Asn
179 445 450 455
181 tcg ctg cgc ttc acc ccg cac ttc ggc atg gac gag gcc gaa ctg gac 2225
182 Ser Leu Arg Phe Thr Pro His Phe Gly Met Asp Glu Ala Glu Leu Asp
183 460 465 470 475
185 ctg ctg gtg gag atg gtc ggg cgt gcg ctg gtc gaa ggc cca cgc ccg 2273
186 Leu Leu Val Glu Met Val Gly Arg Ala Leu Val Glu Gly Pro Arg Arg
187 480 485 490
189 gcc tga tccgcacccg caggacggaa ggcacgagcc caccgtgagg cgggctcttt gc 2331
190 Ala
192 tgcccgccac cagcggcaac aggcgcgct gtcaccggcc aggcggggcg ccggcagtg 2391
194 gtttcagccg caggggtccg ccctgccagc gcctgcggcg gggcacaggc ttgcgggcat 2451
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200 cagcaccatc gggtgcgtga ctgacgcgcc gctggccgtt gcgggacagc agcctttgcg 2631
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204 <210> SEQ ID NO: 2
205 <211> LENGTH: 6357
206 <212> TYPE: DNA
207 <213> ORGANISM: Flavobacterium lutescens
209 <220> FEATURE:

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210 <221> NAME/KEY: CDS

211 <222> LOCATION: (2855)..(4387)

213 <400> SEQUENCE: 2

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218 gcaccacctt ggcgcgaaa taggccagtt cgcaggcctc gtcatactg agcgtggcca 180
220 gggtcaccgc ctcgggcacc acccgcggtt cggcgacag cacaccgtcg acatcggtcc 240
222 agatgtgcag ctcgcccgcc tcgaacagcg cggcaaagat cggcccgaa taatcgctgc 300
224 cgttgcgggc caggttggtg atcctgccct ggccatcac ggcgacaaa ccggtgacca 360
226 ccaccgcga ctgcggttg tccacacgcc aggcggccag gttggcgca ctgcttccc 420
228 agtcgacgt gacccacgc tcgcgtgtg cgaccaccag cacatcgcg gcacgagca 480
230 ccgcgcagg gtggccgagc cggttgaaat agcgcccgag cagctgggc gagaacacct 540
232 cggccagccc ctgcaccctt tcaagacct cctcgggcag gccgcgac accgccagcg 600
234 cttccagcaa cccggccagc ttgtcaaagc gtccatccag ccactgcagc aggtcggcag 660
236 aatcctcgcc cagcagttcg gtggcgctt catggtggcg ctggcgagc gcctgccagg 720
238 catcacgcca gcgcggtga cgtggggcg ccagggtagc cagctcgac aaggcatcg 780
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VERIFICATION SUMMARY

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Input Set : A:\FUJII Sequence listing.txt

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L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date
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L:601 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:621 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:639 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:652 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:9
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Indexing Officer: TROBINSON - TERRI ROBINSON
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No.	Doccode	Number of pages
1	CRFL	6

Total number of pages: 6

Remarks:

Order of re-scan issued on